





Document: D000 (4,448 pages)

**Figure 2B**

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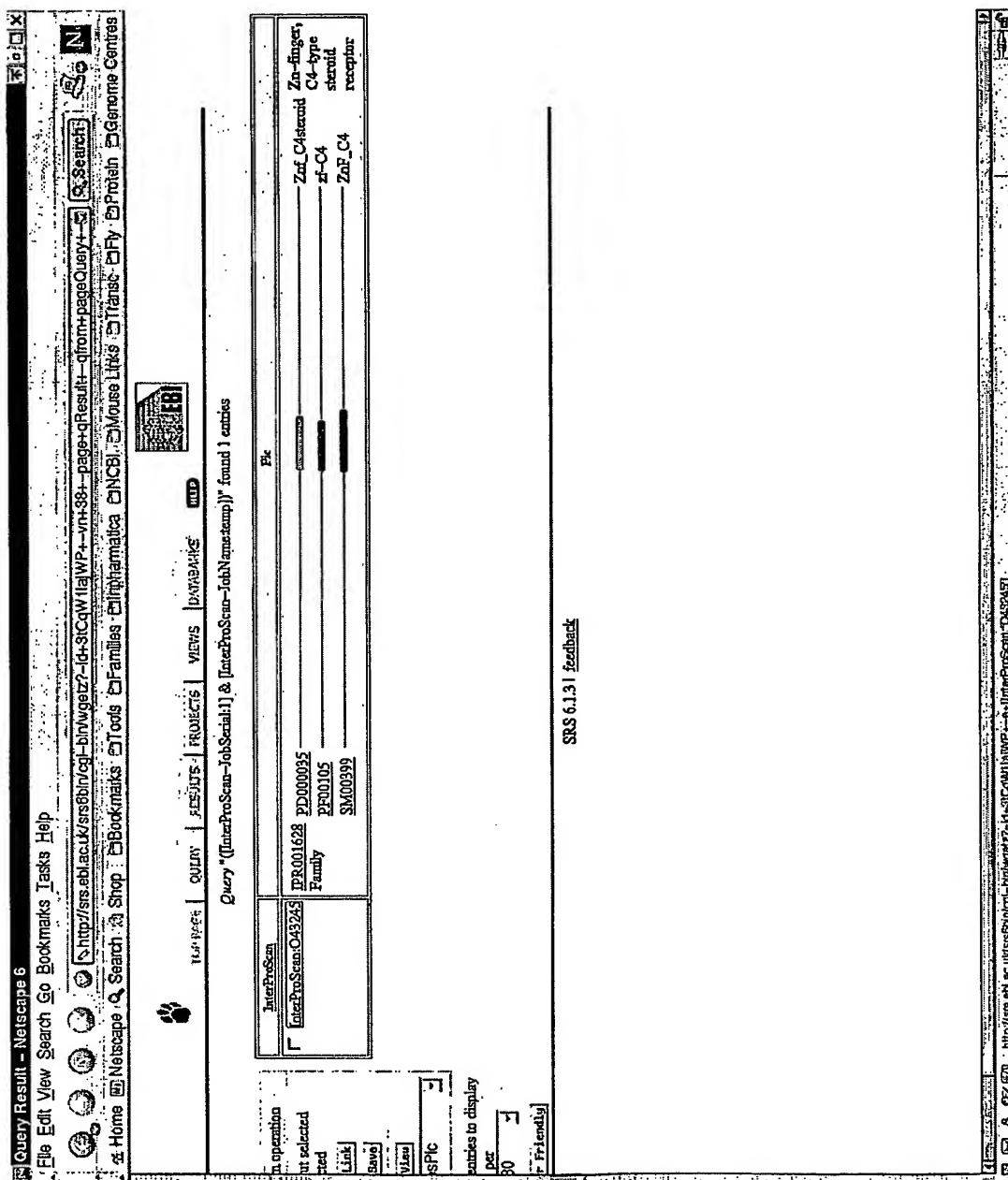
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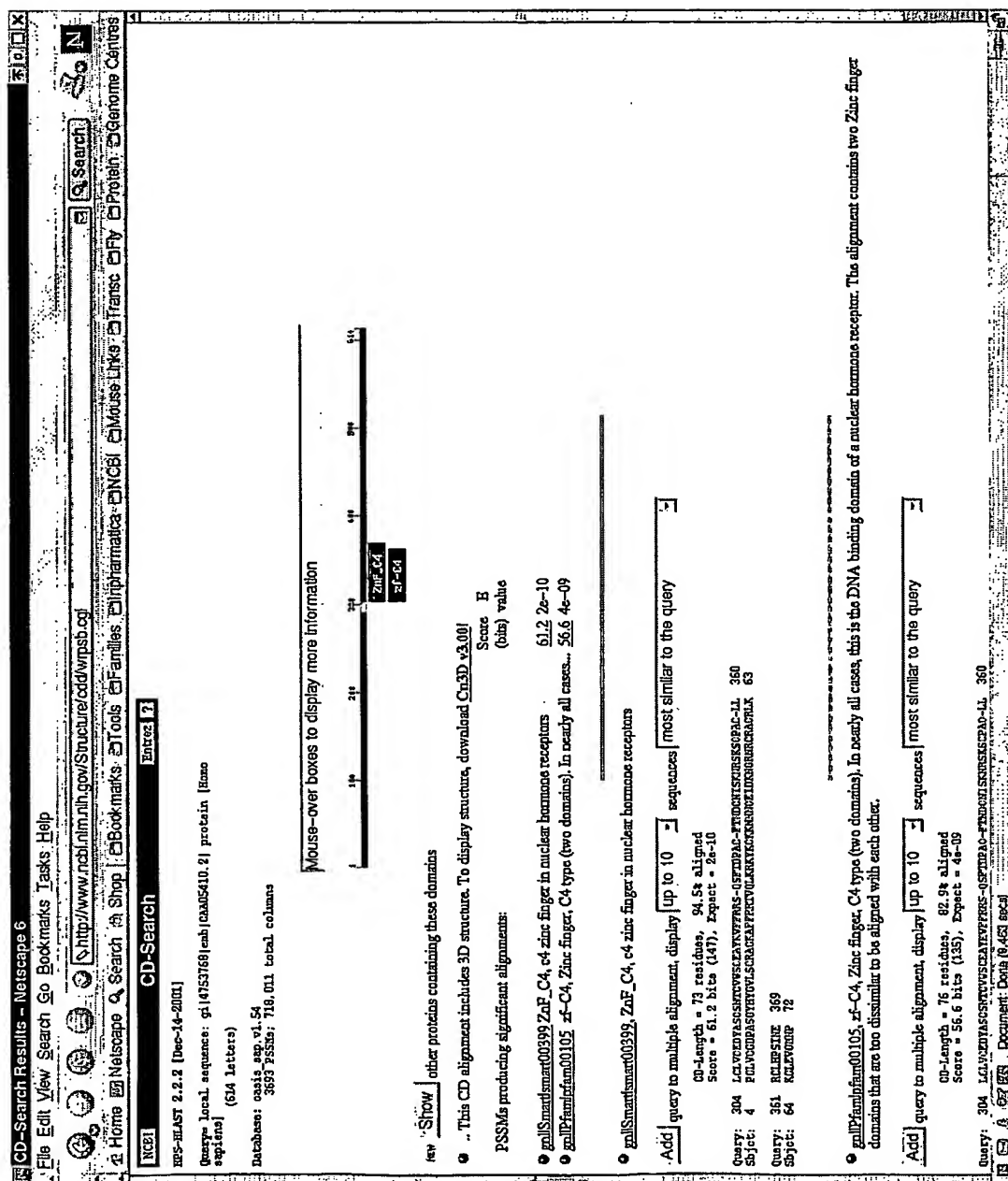
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Figure 2C



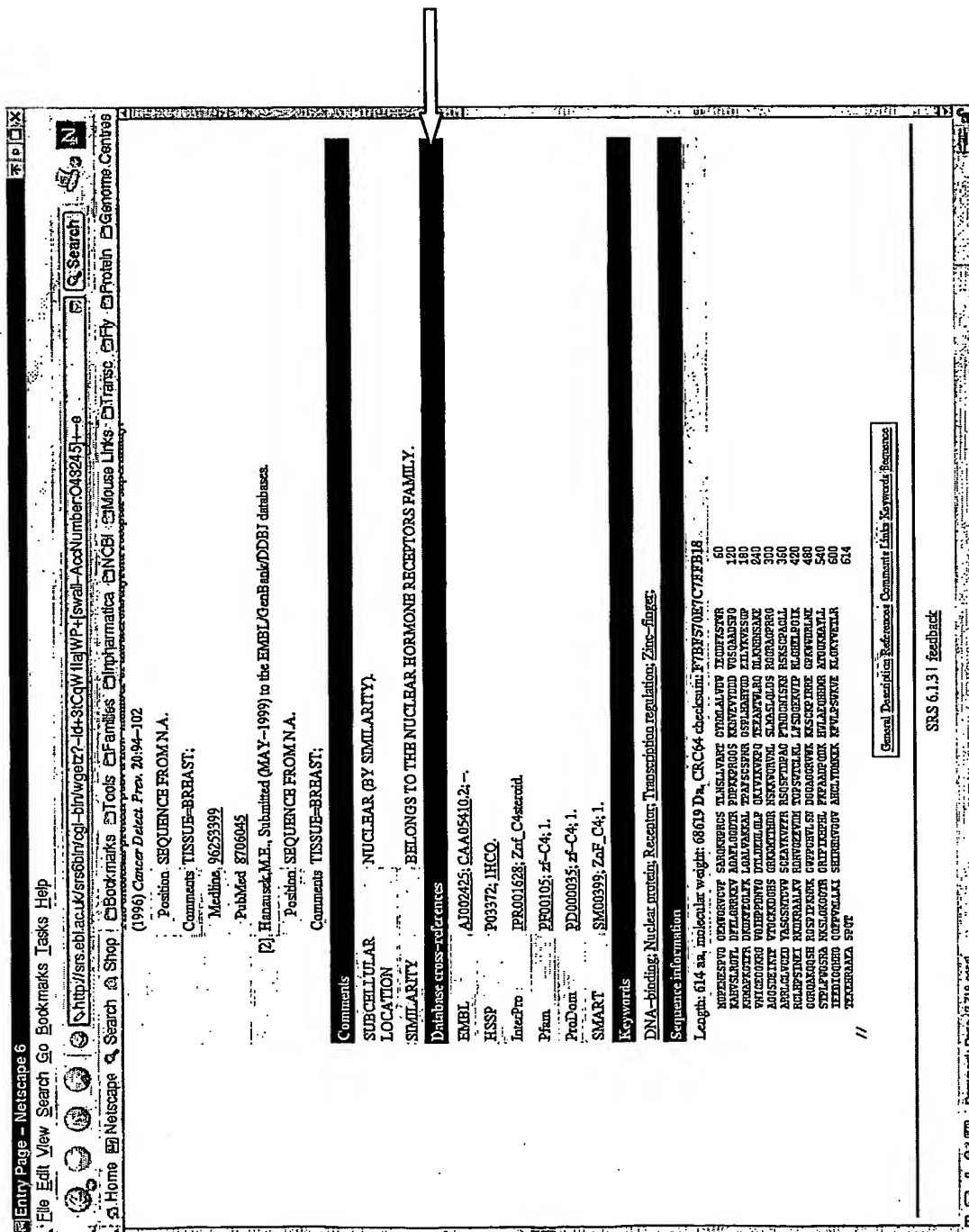
### Figure 3



**Figure 4**

[illegible]

**Figure 5A**



**Figure 5B**

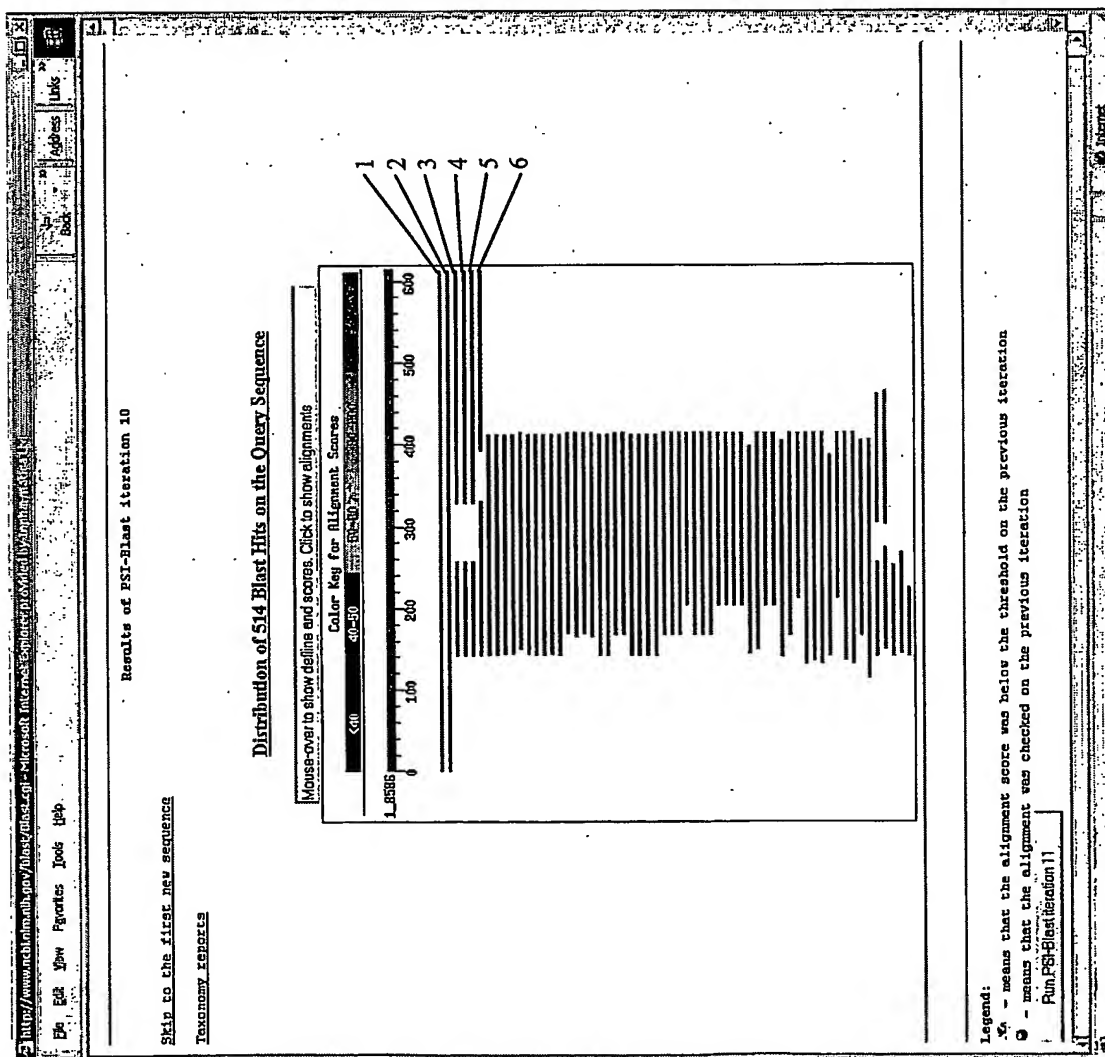
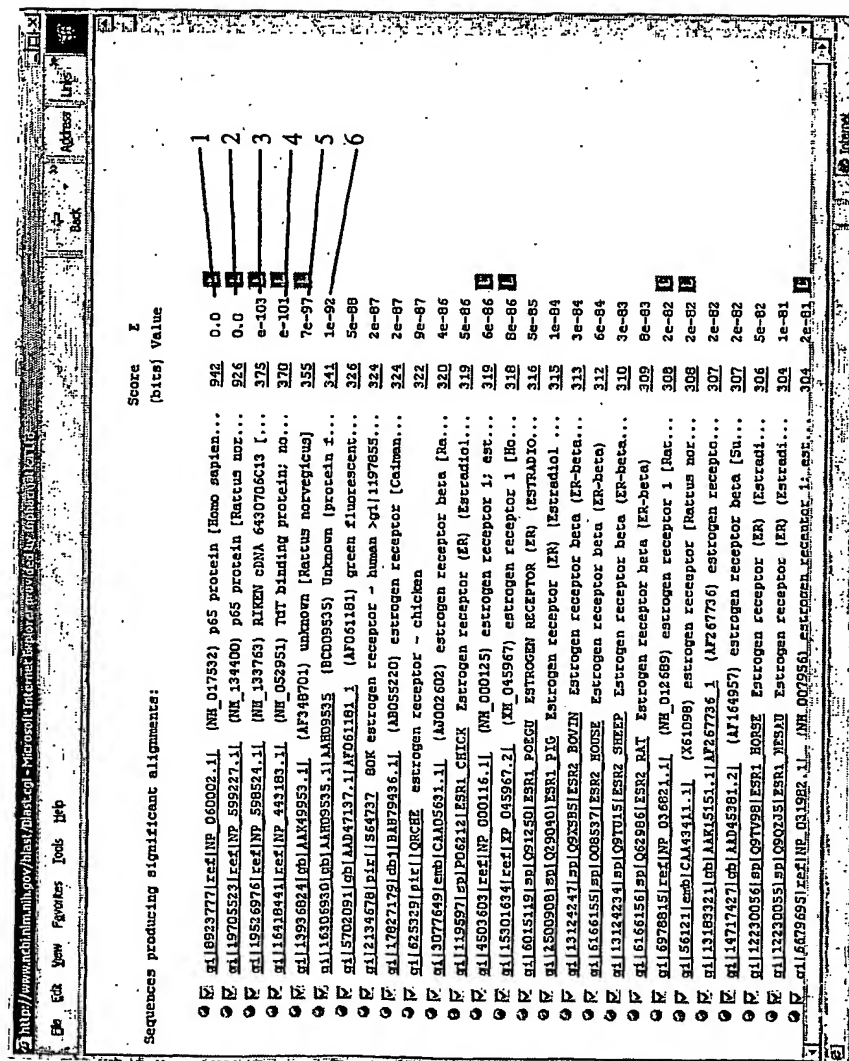


Figure 5C



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Relationship Results

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<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	GenBank	AAA51775.1	androgen receptor	Homo sapiens	918	283-578	535-787	P10275	31	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	GenBank	AA045921.1	androgen receptor	Homo sapiens	906	192-578	410-715	P10275	31	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	SWISS-PROT	P08235	Mineralocorticoid receptor	Homo sapiens (human)	984	67-381	367-683	P08235	34	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	SWISS-PROT	O19052	Proximate proliferator ac...	Oryctolagus cuniculus (Rabbit)	475	216-428	1-243	BAA98100.1	24	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	GenBank	CAB61233.1	peroxisome proliferator ac...	Crocodylus niloticus	393	234-428	6-169	CAB61233.1	24	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	SWISS-PROT	O97776	Androgen receptor (Olfactory)	Gallemus fulvus rollands	884	192-578	366-719	O97776	31	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	SWISS-PROT	P49843	Glucocorticoid receptor (G...)	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)	758	177-577	284-621	P49843	34	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	GenBank	AA052143.1	nuclear orphan receptor H2...	Rattus norvegicus	598	196-599	146-596	AA052143.1	24	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	GenBank	AAA62110.1	PPAR gamma	Mus musculus	475	216-428	1-243	BAA98100.1	24	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	SWISS-PROT	O73673	Glucocorticoid receptor (G...)	Paralichthys olivaceus (Flounder)	807	186-595	331-696	O73673	33	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	GenBank	AA042362.1	progesterone receptor	Xenopus laevis	732	183-577	128-600	AA042362.1	28	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	GenBank	CAB61263.1	peroxisome proliferator ac...	Trachemys scripta elegans	393	274-428	6-169	CAB61263.1	24	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	SWISS-PROT	P49699	Androgen receptor (Olfactory)	Oryctolagus cuniculus (Rabbit)	709	82-578	105-578	P49699	30	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	SWISS-PROT	O29131	Mineralocorticoid receptor	Tupaia glis belagasi (Common tree shrew)	977	67-577	365-345	O29131	34	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	SWISS-PROT	P49700	Ultrashort protein	Bombyx mori (Silk moth)	462	244-396	23-283	P49700	22	2
<a href="#">ES0</a> <a href="#">ESA</a> <a href="#">XR</a> <a href="#">DP</a>	SWISS-PROT	P19091	Androgen receptor	Mus musculus (Mouse)	899	210-578	145-703	P19091	30	2

105 page(s) | 2053 row(s)

CSV Export

Figure 7A

Pharmatica Biopendium TM - Netscape 6  
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Address: http://bpcpr0738080/morphaus2/isp/index.jsp

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### Relationship Results

Accession Code: CAA054102  
Accession Name: Hypothetical protein

RMORBI PSI-BLAST Results

Search in: Source DB column for Prev Next

PAGES: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 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2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2

CAA05410.2 3ERT	MGPENESVGGEMWGRVCFVSARQKPRCSTINSLVARTCYNMIALVDWIEQDFKSTWR 60 -----
CAA05410.2 3ERT	KAHVSRLRGELDFELGRKEVAGAFGLGDFRDPKPKRGSKKNVEVYDDDVGSQAADSPG 120 -----
CAA05410.2 3ERT	KRMAPKGTFRDKDKFEGLFKLGALVAKKALTPAFSCSPNRGSPHHAHYDELIYKVESGP 180 -----
CAA05410.2 3ERT	VNICEGKRGVGIHPPDPNYGDTLDENLGLPQKIVIKVPQTEEANTWLRQDLKNHNSAKE 240 -----
CAA05410.2 3ERT	AGGSDEIKTFVTGCKKGSHGRKNMTTHDRNSKKWQVNLISMASLQLDSRGRAGPRRG 300 -----
CAA05410.2 3ERT	ARRLCLVCEDIYASCSNTCVWCEAYKVFRRSQSFTDPACFTDNCISKNRSKSCPACLL 360 -----
CAA05410.2 3ERT	RCLHPSINEIRKDKRAALKVRDVGVEVDMTGPSWTCLLLESDGEKVPRLGHELPGIK 420 -----LALSLTADQMVSAALLDAEPILYSEYDPTFPFSEASMGLL 346
CAA05410.2 3ERT	GGRQAKQQSHRGSPIPKNRKGWPPGHVLSNDGGAGGRVWKKKCKPIREGPKWWDRLN- 479 TNLADREL VH-MINWAKRVPGFVDLTLDQVHLLECAWLEILMIGLVWRSMEHPGKLLFA 405
CAA05410.2 3ERT	-----ESTPLFWGSRANKSLGKGTRGRIFIKHPLHFKFAADPQDK-- 520 PNLLLDNRNQKCVGMEVIFDMLLATSS--RFRMNLQGEFVCLKSIILLNSGVYTFLS 463
CAA05410.2 3ERT	---HWLAEQHHMRATGGK---MAYLLIEEDIG-CHHGCGFPVMTLKIISHIRHMVGGVAH 572 STLKSLEEKDHIHRVLDKITDTLILHMAKAGLTLCQOHQRLAQLLILSHIRHMSNKGME 523 *****DIMER HELIX*****
CAA05410.2 3ERT	CLYDMKEKFKVLPWVKVEKLGKVVETLRTKEHRAAEASPQT 614 HLYISMCKKNVVP---LYDLLLEMLDAHRLHAP----- 552 ***

Figure 8: Genome Threader alignment (3ERT numbering corresponds to position in the full-length sequence rather than crystallised domain)

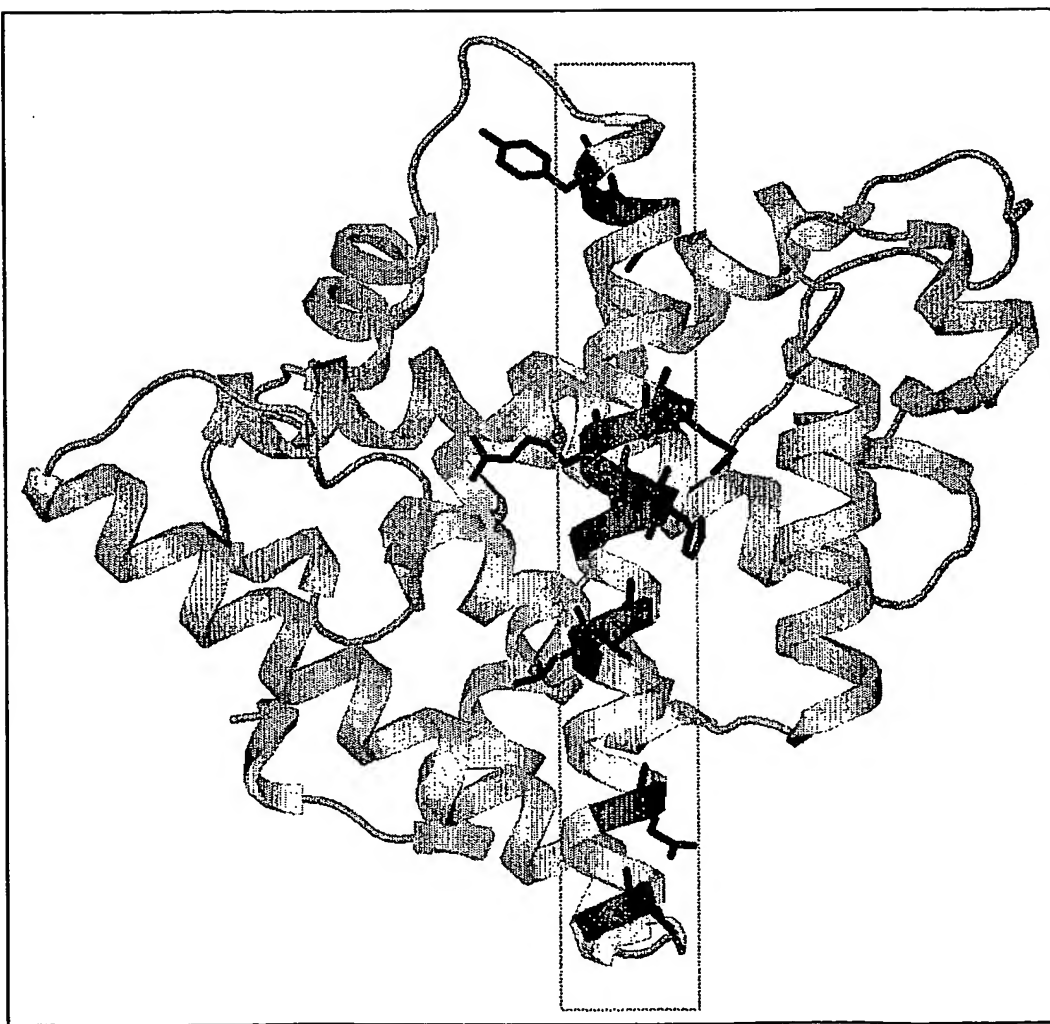


Figure 9: Dimerisation helix is enclosed in dotted box.

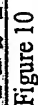


Figure 11

**Figure 12**

3ERT	-----	MDPENVRAEGGDMREKVRLLSSARQ-RLRCSTKNSLLIVARTC--VLRIVDWIEQDLKSTCE	57
CAA05409.2		MGPENESVPGGEMWGRVCVFSARQKRPRCSTLNSLLVARTCYNMLALVDWIEQDFKSTWR	60
CAA05410.2		-----	
3ERT	-----	KAHVSLRGYLDLQCCGRRRKEVAGA-LGGDTRDPKPKPRGGSKKNVEVYGGDDVGSQAADS	116
CAA05409.2		KAHVSLRGFLDFEL--GRRKEVAGAFGLGGDTRDPKPKPRGGSKKNVEVYDDDDVGSQAADS	118
CAA05410.2		-----	
3ERT	-----	PRKQLAAKGTFRDKDKIEALFKLGELVAKKALSSAITWFPNSVSPLHAHYGDEILYKDES	176
CAA05409.2		PGKRMAPKGTFRDKDKFEGLFKLGALVAKKALTAFSCSPNRGSPPLHAHYGDEILYKVES	178
CAA05410.2		-----	
3ERT	-----	GLVNISEGGKRGVEIHPPDNFGITTLDEDLGFPQIIVINVKPQTEEANTWYRQDLKYHNS	236
CAA05409.2		GPVNICEGGKRGVGIHPPDNYG-DTLDENLGLPQKIVIKVKPQTEEANTWLRQDLKNHNS	237
CAA05410.2		-----	
3ERT	-----	ANEAGYSDENKTFVRGCRKDGHSERNNMTTGDRNSKKAQPVNFSLMASLALDSRGKAAGP	296
CAA05409.2		AKEAGGSDEIKTFVTGCKKDGHSGRKNMTHDRNSKKWQVRVNLISMASLQLD SRGGRAGE	297
CAA05410.2		-----	
3ERT	-----	RRGARRLCLVCEDYASCSNTCVWSCEAYKVFFRRSQSFTDPACFTNDCNISKNRSKSCPA	356
CAA05409.2		RRGARRLCLVCEDYASCSNTCVWSCEAYKVFFRRSQSFTDPACFTNDCNISKNRSKSCPA	357
CAA05410.2		-----	
3ERT	-----	-----LALSLTADQMVSAALLDAEPPILYSEYDPTTRPFSEASMM	343
CAA05409.2		CLLRLCLQPSINEIRKDKRAALNVRDNGVEEVDMTGPSWTCCLKLLFSDGKVIPLRLAHELP	416
CAA05410.2		CLLRLCLHPSINEIRKDKRAALKVRDNGVEEVDMTGPSWTCCLKLLFSDGKVIPLRLGHELP	417

Figure 13 Part I

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3ERT      GLLTNLADREL VH-MINWAKRVPGFVDLTLLHDQVHLLLECAWLEILMIGLVWRSMEHPGKL 402
CAA05409.2 GIKRGRQAEESHRGSPIPKKRKGWPPGHVLSNDRAAAGTVWPKSCPEIRREGPKWDAR 476
CAA05410.2 GIKGGRQAKQQSHRGSPIPKNRKGWPPGHVLSNDGAGGRVWKKKCKPIRREGPKWDR 477

3ERT      LFAPNLLLDRNQKCVGMVEIFDMLLATSS--RFRMNLQGEFEVCLKSIILLNSGVYT 460
CAA05409.2 LN-----ESTTFVLGSRANKALGKGTRGRIYIKHPHLFKYAADPQD 518
CAA05410.2 LN-----ESTPLFWGSRANKSLGKGTRGRIFIKHPHLFKFAADPQD 519

3ERT      FLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLLQQHQRLAQLLLLSHIRHMSNK 520
CAA05409.2 K-----HWLAEQQLHMRATGGK----MAYLLIEEDIE-QHHGQRFVAVELLKISHIRHMVEG 568
CAA05410.2 K-----HWLAEQQLHMRATGGK----MAYLLIEEDIG-QHHGQGFVPMLLKISHIRHMVGG 569
          *****DIMER HELIX*****

3ERT      GMEHLYSMCKKNVVP---LYDLLLEMLDAHRLHAP----- 552
CAA05409.2 VAHCLYDMKVIQFVLPSWKVEKLRKYVETLRTENEHRAAEASPQT 613
CAA05410.2 VAHCLYDMKEKKFVLPSWKVEKLRKYVETLRTETEKEHRAAEASPQT 614
          *****

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Figure 13 Part II

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http://srs.abl.ac.uk/srs6html.cgi-bin/wget?-(G-3CQW-ILURXC--e-InterProScan%27O5474S%27)

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This entry is from:

InterProScan

Scan

Link

InterPro friendly

Protein

2b-finger, C4-type serine/threonine (family)

PRODOM: P200055 Znf\_Octadec

PFAM: PF00103 Znf-C1

SMART: SM00393 Znf\_C1

Q5H745 OS: HMAS Length: 613 aa ID: Q5H745 DA: I23C87D

302-357T

302-357T

301-357T

SRS 613 | feedback

Document Done (1325 sers)

Figure 14

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http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi

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CD-Search Entrez 1

RPC-AST 2.2.2 [Dec-14-2001]  
Query: Local sequence: gi14753887|emb|DAM05409.2| p65 protein  
(Rattus norvegicus)  
(613 letters)  
Database: opls's app. v1.54  
3693 PSSM; 716,011 total columns

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190 210 230 250 270 290 310 330 350 370 390 410 430 450 470 490 510 530 550 570 590 610 630 650 670 690 710 730 750 770 790 810 830 850 870 890 910 930 950 970 990 1010 1030 1050 1070 1090 1110 1130 1150 1170 1190 1210 1230 1250 1270 1290 1310 1330 1350 1370 1390 1410 1430 1450 1470 1490 1510 1530 1550 1570 1590 1610 1630 1650 1670 1690 1710 1730 1750 1770 1790 1810 1830 1850 1870 1890 1910 1930 1950 1970 1990 2010 2030 2050 2070 2090 2110 2130 2150 2170 2190 2210 2230 2250 2270 2290 2310 2330 2350 2370 2390 2410 2430 2450 2470 2490 2510 2530 2550 2570 2590 2610 2630 2650 2670 2690 2710 2730 2750 2770 2790 2810 2830 2850 2870 2890 2910 2930 2950 2970 2990 3010 3030 3050 3070 3090 3110 3130 3150 3170 3190 3210 3230 3250 3270 3290 3310 3330 3350 3370 3390 3410 3430 3450 3470 3490 3510 3530 3550 3570 3590 3610 3630 3650 3670 3690 3710 3730 3750 3770 3790 3810 3830 3850 3870 3890 3910 3930 3950 3970 3990 4010 4030 4050 4070 4090 4110 4130 4150 4170 4190 4210 4230 4250 4270 4290 4310 4330 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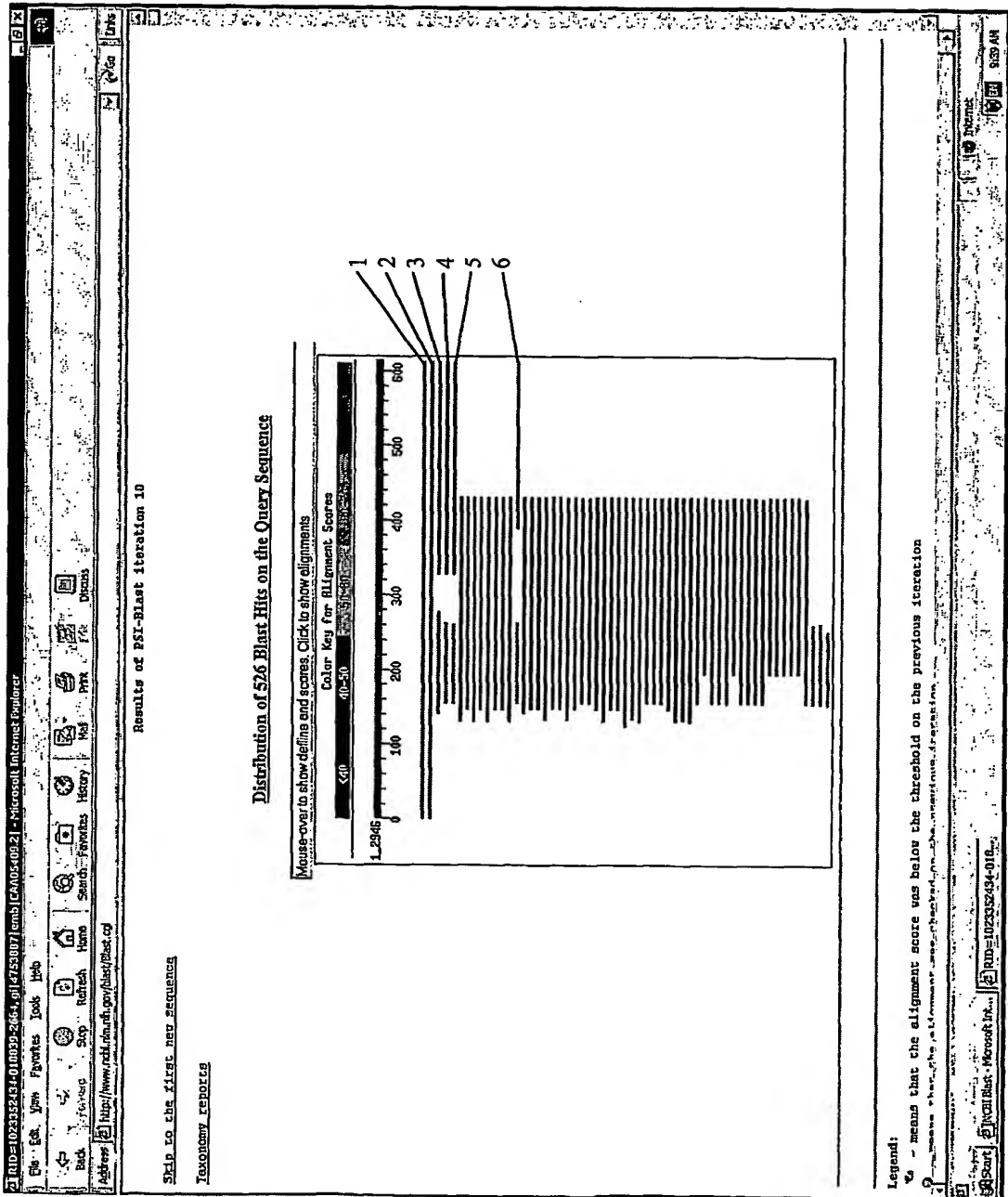
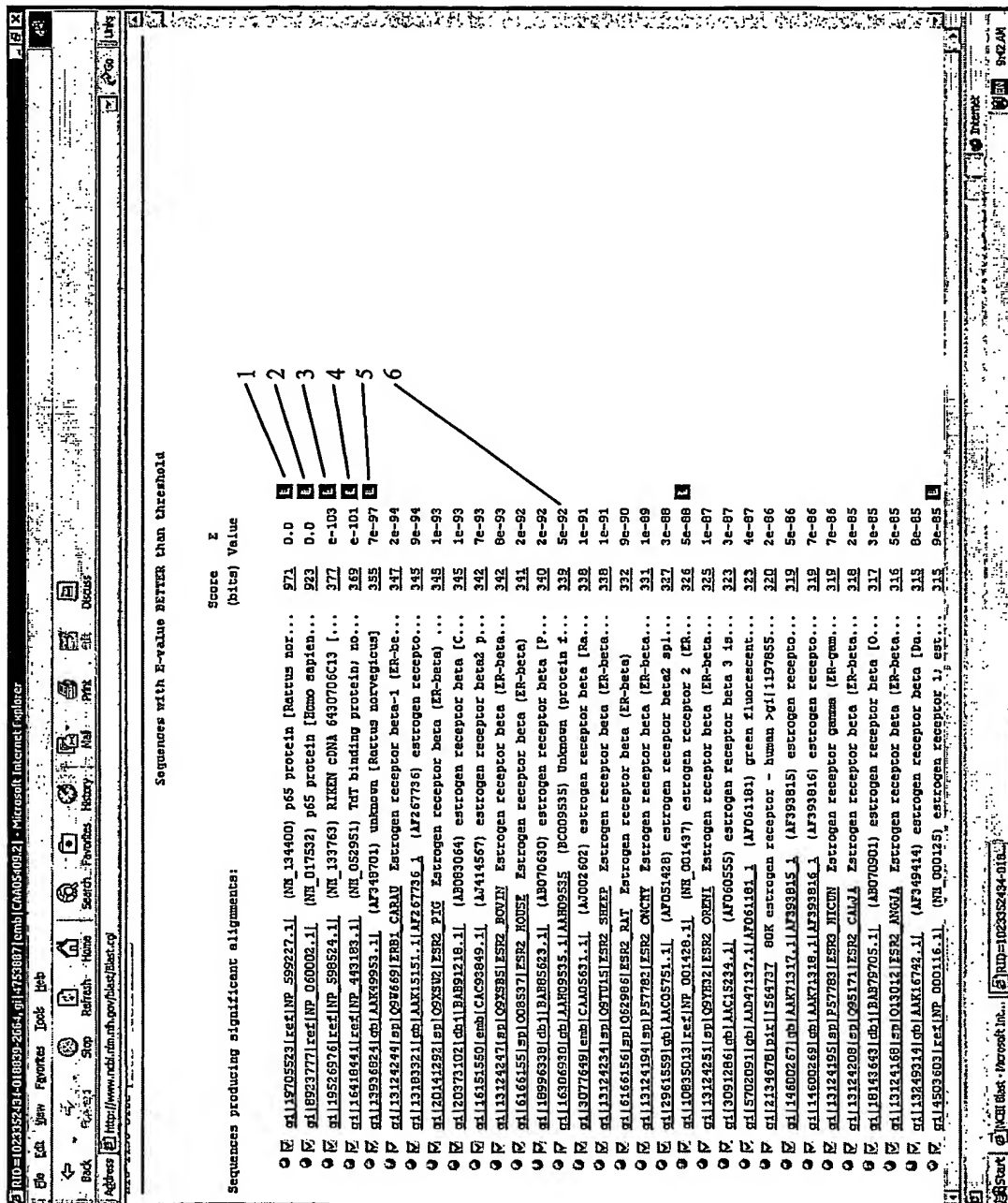


Figure 16A



NCBI Sequence Viewer - Netscape 6  
File Edit View Search Go Bookmarks Tasks Help  
http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=protein&list\_uids=4753887&dopt=GenPept  
Search  
Home Netscape Search Shop Bookmarks

1: CA05409: p53 protein [Rat-16473387]  
Linear ROD 04-MAY-1999

LOCUS CA05409 613 aa linear ROD 04-MAY-1999  
DEFINITION p53 protein [Rattus norvegicus].  
ACCESSION CA05409  
VERSION 2.0  
KEYWORDS  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
(Residues 1 to 613)  
AUTHORS Hanussek K.E., Adams A.K. and Walasek S.  
TITLE The oncofetal protein p53: a new member of the steroid/thyroid receptor superfamily  
JOURNAL Cancer Detect. Prev. 20 (2), 94-102 (1995)  
MEDLINE 9525399  
REFERENCE 2 (residues 1 to 613)  
Hanussek K.E.  
Direct Submission  
Submitted (04-MAY-1997) Hanussek K.E., Carcinogenesis, University of Texas M.D. Anderson Cancer Center, P. O. Box 359, Saltville, Texas, 78577, USA  
REMARK revised by [3]  
REFERENCE 3 (residues 1 to 613)  
Hanussek K.E.  
Direct Submission  
Submitted (04-MAY-1997) Hanussek K.E., Carcinogenesis, University of Texas M.D. Anderson Cancer Center, P. O. Box 359, Saltville, Texas, 78577, USA  
REMARK revised by [4]  
REFERENCE 4 (residues 1 to 613)  
Hanussek K.E.  
Direct Submission  
Submitted (04-MAY-1999) Hanussek K.E., Carcinogenesis, University of Texas M.D. Anderson Cancer Center, P. O. Box 359, Saltville, Texas, 78577, USA  
CONCEPT On May 5, 1999 this sequence version replaced gi:268717.  
FEATURES  
source  
1..613  
/organism="Rattus norvegicus"  
/strain="Fisher 344"  
/db\_xref="taxon:10116"  
/call\_line="T52 Hepatocarcinoma"  
Protein  
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CDS  
1..613  
/coded\_by="A1002424.2:107..1948"

ORIGIN  
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61 valtying acgcttga gaaagcttpa ptagagaa mnyvdydy aqadspiq  
121 taagftrk tctatfag tctatfag tctatfag tctatfag tctatfag  
181 taagftrk tctatfag tctatfag tctatfag tctatfag tctatfag  
241 gyaaktkf tctatfag tctatfag tctatfag tctatfag tctatfag  
301 rrlclvady tctatfag tctatfag tctatfag tctatfag tctatfag  
361 clapalnir ktraaalnr dngvsvat gactclll fadnkvpr lhaalpvkr  
421 gyaacvahr gypvldkq vpyvnlnd tcaatvtpk kaccpirrg phndalnas  
481 ttfvlgarn kalgvarg rylvaphl fyadqgqb elaaqlara tpycaaylli  
541 eedatqhg rtrvllkis klfmavga hclvkvvq fclpavvkv lkyvratlr  
601 enacvaaa ptt  
//

Figure 17

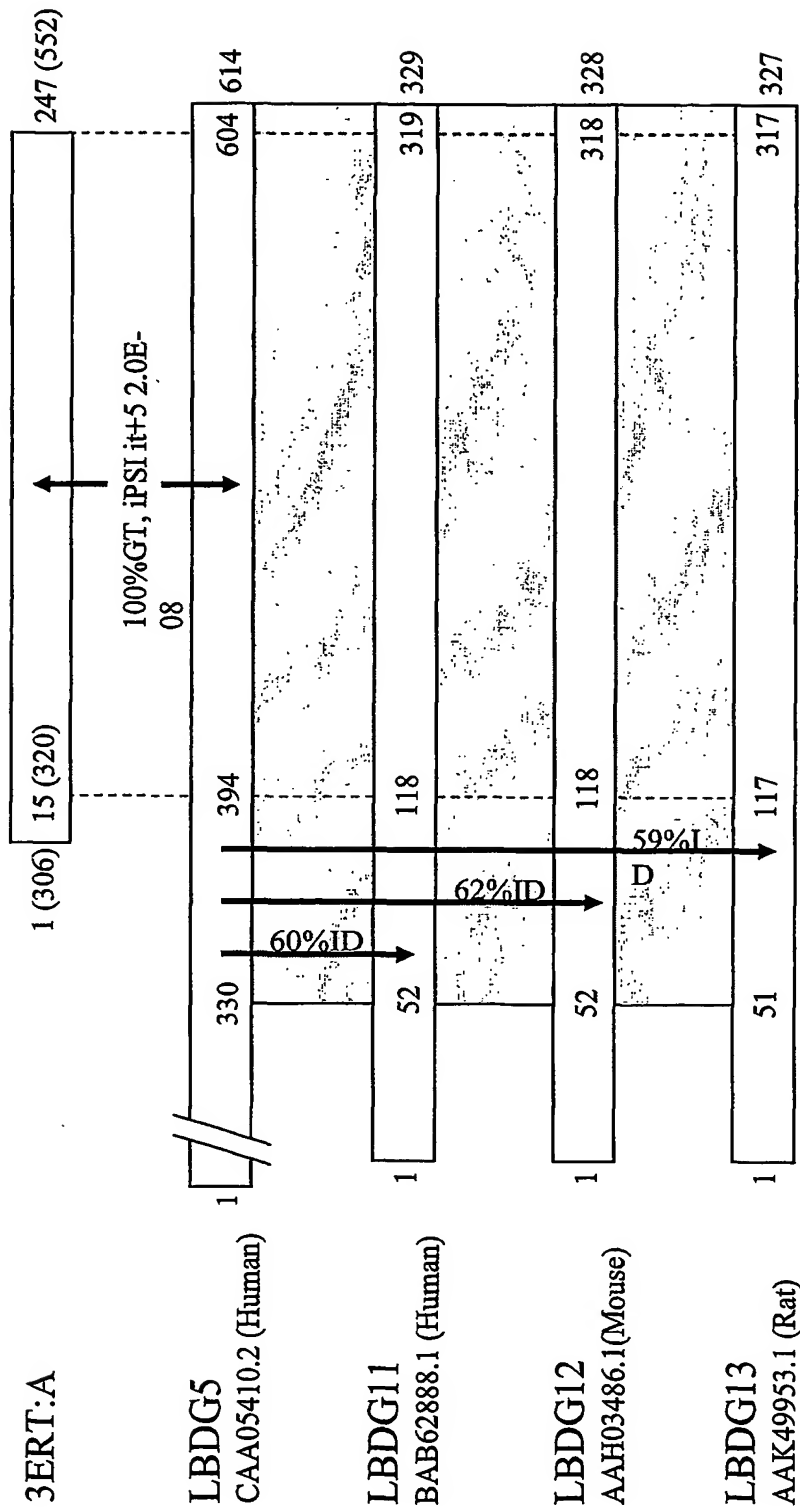


Figure 18: relationships between 3ERT:A, CAA05410.2 (LBDG5), BAB62888.1 (LBDG11), AAH03486.1 (LBDG12) and AAK49953.1 (LBDG13).



3ERT		MIGLVWRSMEHPG-KLLFAPNLLLDNRQKGCVEGMVEIFDMLLATSS--RFRMNLQEE	444
CAA05410.2	(LBDG5)	SCKPIRREGPKWW-DRLN-----ESTPLFWGSRANKSLGKGGRGRI	503
BAB62888.1	(LBDG11)	SCEPIRREGPKWDPARLN-----ESTTFLGSRANKALGMGGTRGRI	232
AAH03486.1	(LBDG12)	SCEPIRREGPKWDPARLN-----ESTTFLGSRANKALGMGGTRGRI	231
AAK49953.1	(LBDG13)	SCEPIRREGPKWDPARLN-----ESTTFLGSRANKALGMGGTRGRI	230
3ERT		FVCLKSIILNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMKAGLTQQQHQL	504
CAA05410.2	(LBDG5)	FIKHPHLFKFAADPQDK-----HWLAEQHHMRATGGK---MAYLLIEEDIG-QHHGQGF	553
BAB62888.1	(LBDG11)	YIKHPHLFKYAADPQDK-----HWLAEQHHMRATGGK---MAYLLIEEDIR-D-----	276
AAH03486.1	(LBDG12)	YIKHPHLFKYAADPQDK-----HWLAEQHHMRATGGK---MAYLLIEEDIR-D-----	275
AAK49953.1	(LBDG13)	YIKHPHLFKYAADPQDK-----HWLAEQHHMRATGGK---MAYLLIEEDIR-D-----	274
3ERT		AQLLLILSHIRHMSNKGMEHLYSMK---CKNVVP---LYDLLLLEMLDAHRLHAB	552
CAA05410.2	(LBDG5)	PVMLLKISHIRHVMVGVAHCLYDMK---EKKFVLPSWKVEKLGKYVETLRTKEHRAAEA	610
BAB62888.1	(LBDG11)	---LAASDDYR-----GCL-DLKLEELKSFVLPSWMVEKMRKYMETLRTENEHRAVEA	325
AAH03486.1	(LBDG12)	---LAASDDYR-----GCL-DLKLEELKSFVLPSWMVEKMRKYMETLRTENEHRAVEA	324
AAK49953.1	(LBDG13)	---LAASDDYR-----GCL-DLKLEELKSFVLPSWMVEKMRKYMETLRTENEHRAVEA	323
3ERT		----	552
CAA05410.2	(LBDG5)	SPQT	614
BAB62888.1	(LBDG11)	PPQT	329
AAH03486.1	(LBDG12)	PPQT	328
AAK49953.1	(LBDG13)	TPQT	327

Figure 19 PartII

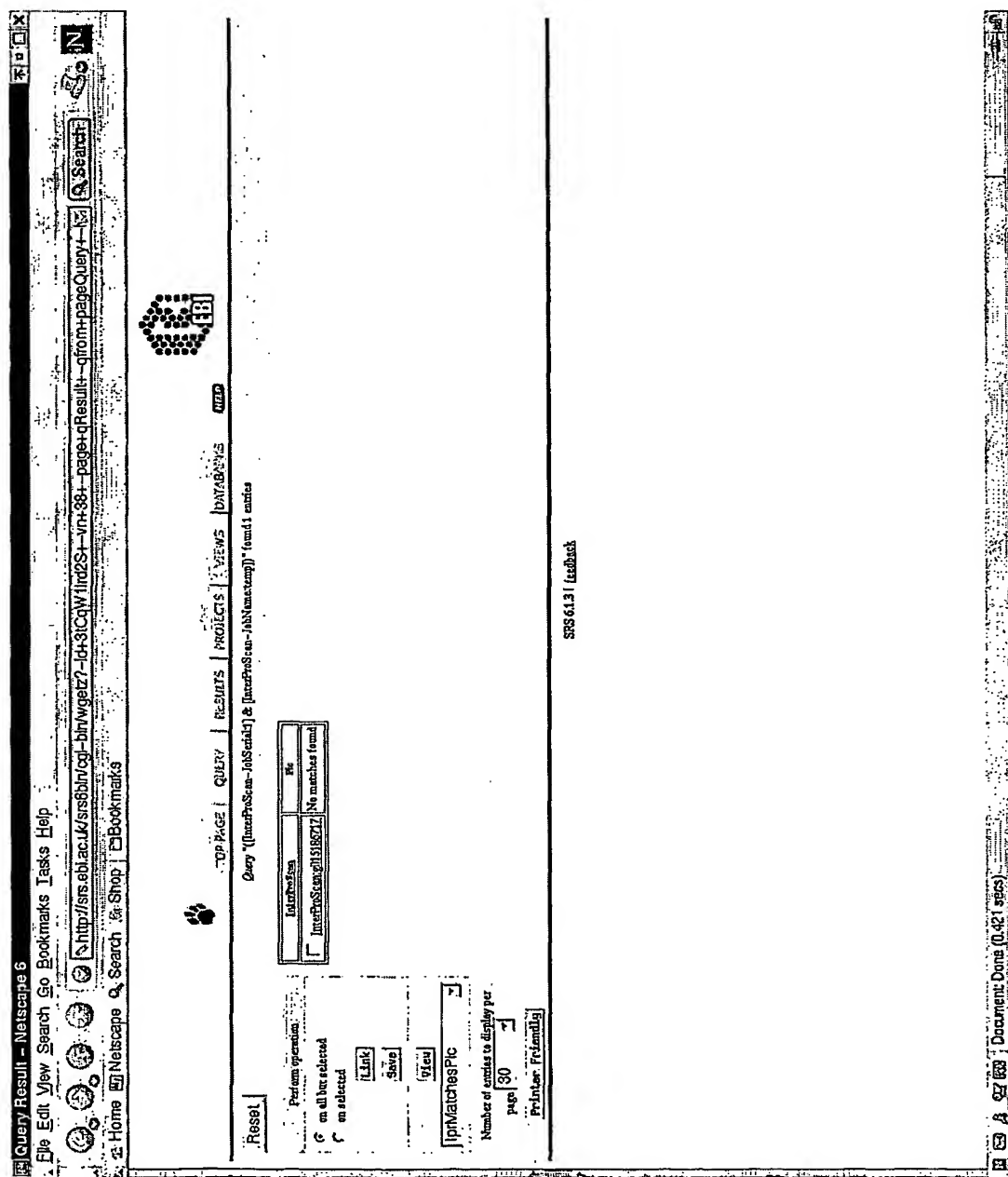


Figure 20

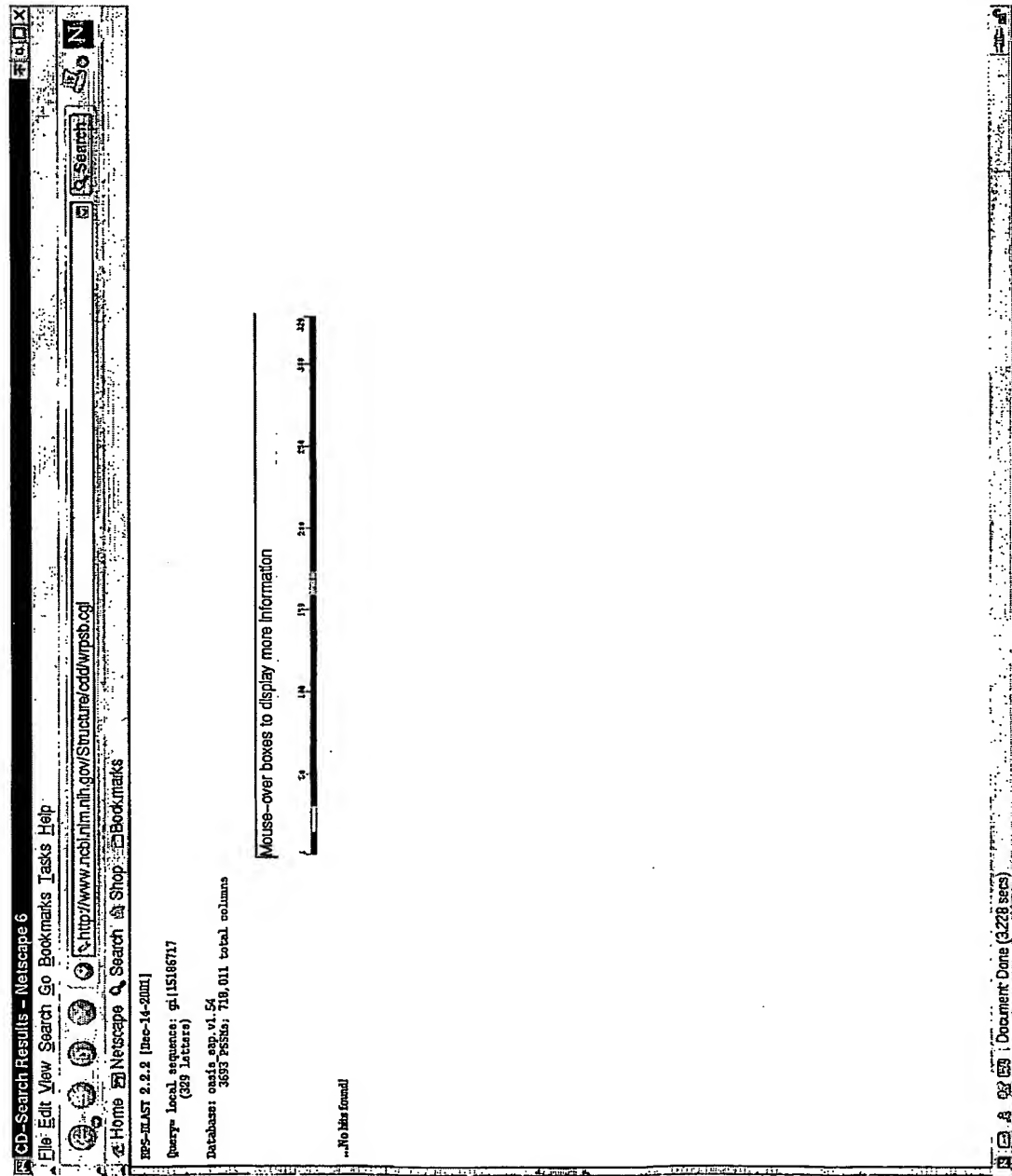


Figure 21

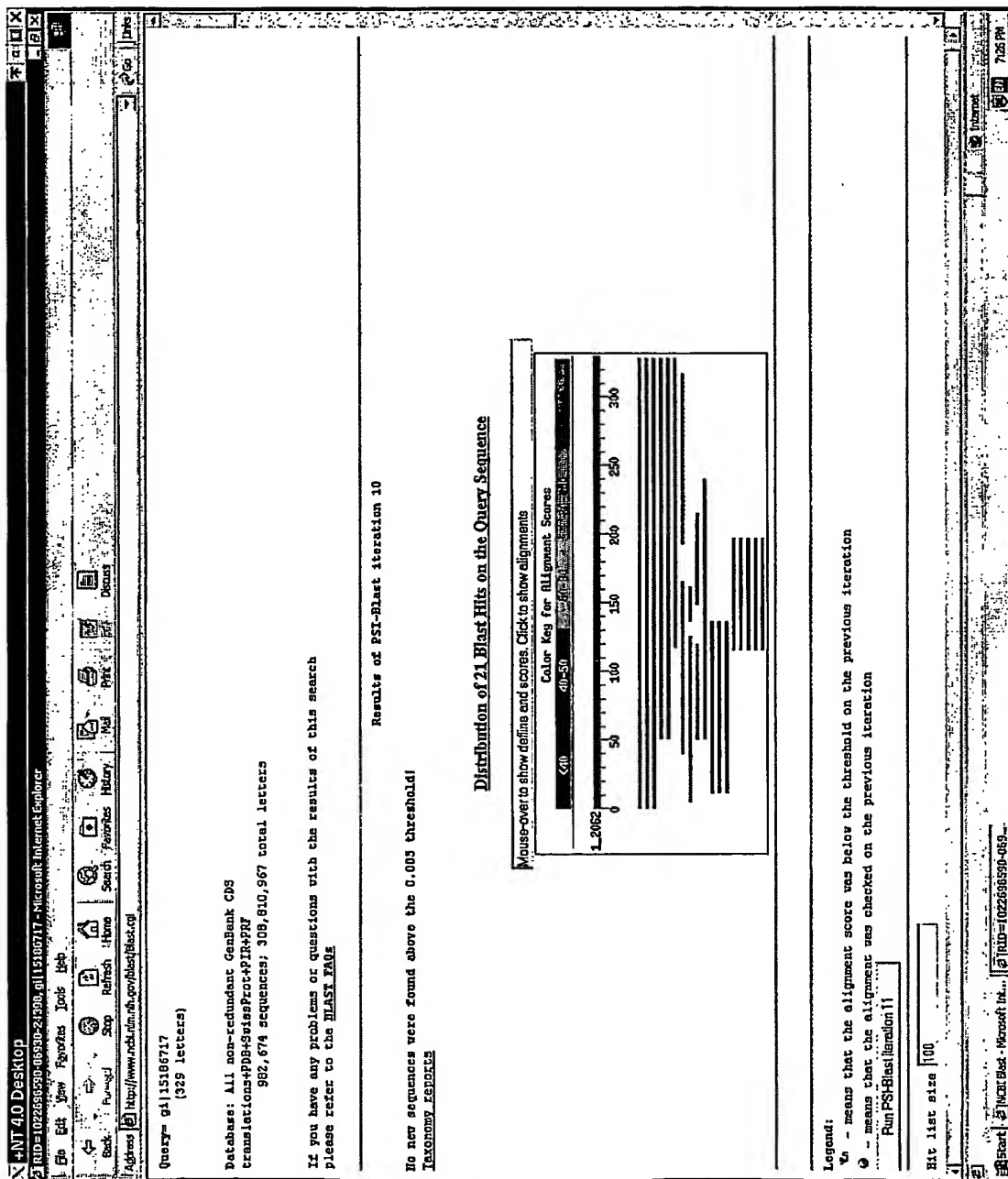


Figure 22

NT 4.0 Desktop  
RID=102209590-06930-24990.gli15100717 - Microsoft Internet Explorer  
File Edit View Favorites Tools Help  
Back Forward Stop Refresh Home Search Favorites History Mail Print Windows  
Address http://www.ncbi.nlm.nih.gov/blast/blast.cgi  
U - means that the alignment was checked on the previous iteration  
Run PSI-Blast iteration 11

Hit list size 100

Sequences producing significant alignments:

	Score	E
	(bits)	Value
gi116410441 ref NP_443183.1  (NH_052951) Tat binding protein; no...	512	e-174
gi119526976 ref NP_59524.1  (NH_133763) RIKEN cDNA 643070G13 [...]	506	e-173
gi113936824 emb AA04953.1  (AF348701) unknown [Rattus norvegicus]	506	e-167
gi119705523 ref NP_59527.1  (NH_134400) p65 protein [Rattus norvegicus]	428	e-119
gi118923777 ref NP_060002.1  (NH_017532) p65 protein [Homo sapiens]	412	e-114
gi116906930 emb AA09595.1 AA09595 (BC009535) Unknown protein f...	397	e-110
gi111465971 emb CAC17442.1  (AL050348) d4447F3.4.2 (novel prot...	235	3e-61
gi113559286 emb CAC36107.1  (AL050348) d4447F3.4.3 (novel prot...	225	6e-58
gi117922271 emb AA047876.1  (AL050348) d4447F3.4.3 (novel prot...	190	2e-47
gi117903421 emb AA047194.2  (S82307) p65 [Homo sapiens]	85	1e-15

Sequences with E-value WORSE than threshold

Sequences producing significant alignments:

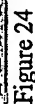
	Score	E
	(bits)	Value
gi117555590 ref NP_499042.1  (NH_066641) T2305.6.p [Caenorhabditis...]	41	0.023
gi119256911 emb AA06997.1 AC005292 F26724.8 [Arabidopsis...]	38	0.14
gi118220680 ref NP_173737.1  (NH_102172) conserved hypothetical ...	38	0.14
gi118220680 ref NP_173737.1  (NH_102172) conserved hypothetical ...	38	0.14
gi117026228 emb CAC63682.1  (AJ305314) hypothetical protein [Acetab...	34	2.1
gi117148513 emb CA012729.1  (AJ420810) ADAMTS-13 protein [Homo s...	34	2.6
gi118571521 ref XP_008414.1  (X008414) a disintegrin-like and ...	34	2.7
gi115963593 emb AA11095.1 AF414401 ADAMTS13 [Homo s...	34	2.8
gi117148513 emb CA012729.1  (AJ420810) ADAMTS-13 protein, trunca...	34	3.0
gi115888941 ref NP_354622.1  (NC_003062) ACR_C_3005p [Agrobacter...	33	5.6
gi118225111 ref NP_080605.1  (NH_018195) mitochondrial ribosomal ...	32	6.1

Sequences with E-value WORSE than threshold

Run PSI-Blast iteration 11

US Star | Microsoft Internet Explorer | http://www.ncbi.nlm.nih.gov/blast/blast.cgi | 7/28/04

Figure 23



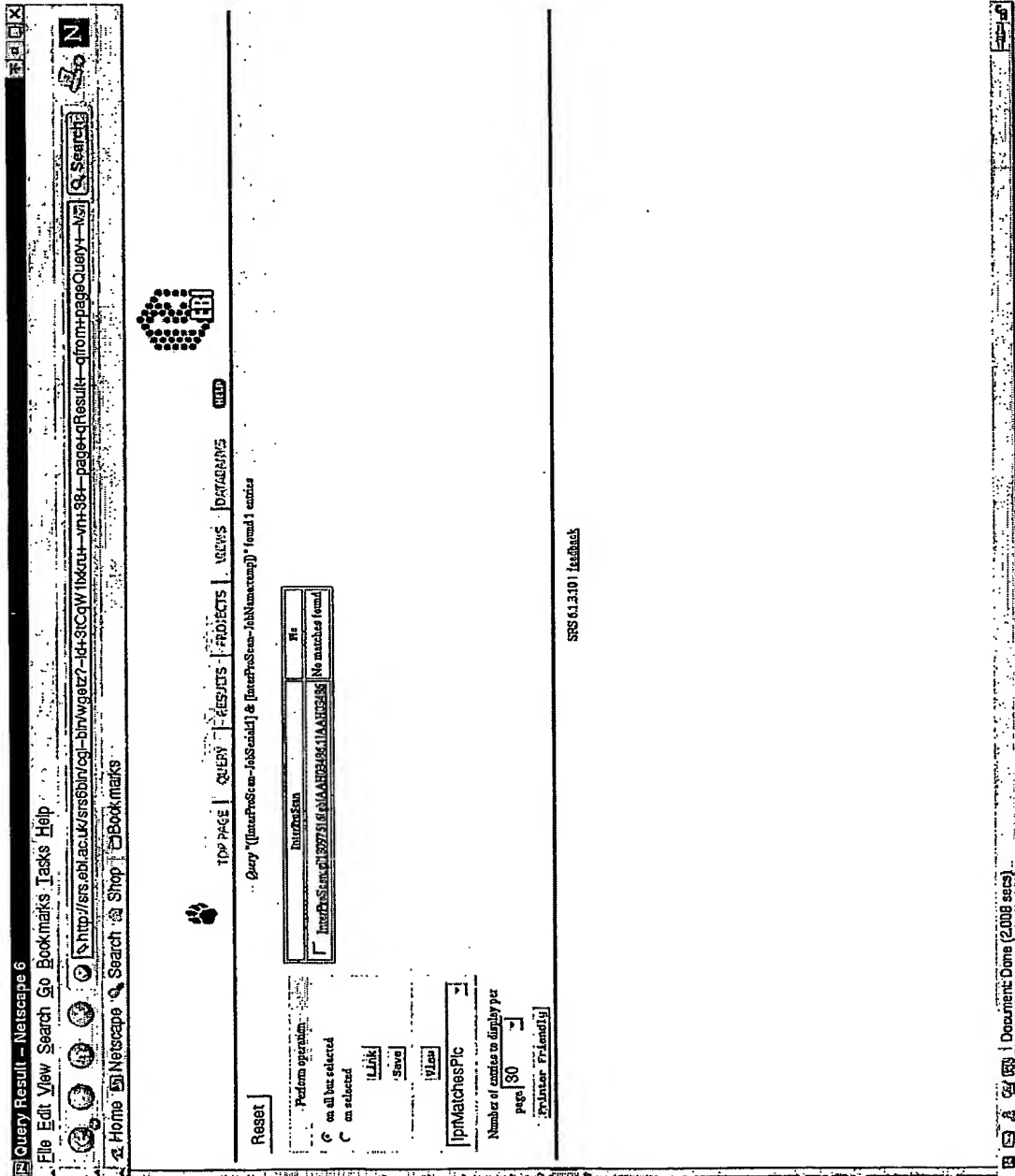


Figure 25

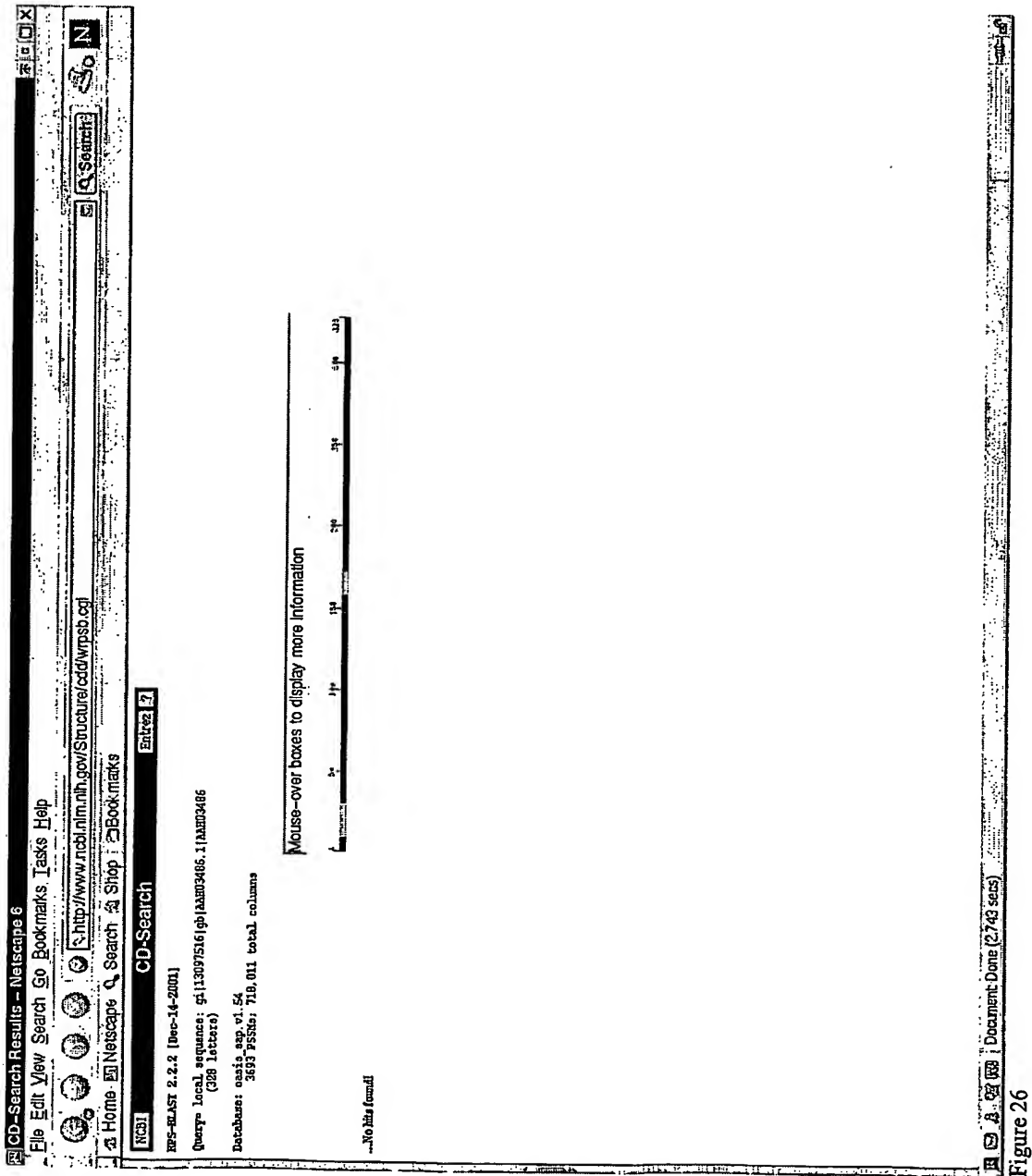


Figure 26



Address: http://www.ncbi.nlm.nih.gov/blast/blast.cgi

Sequences producing significant alignments:

Score	E	(bits) Value
584	e-166	
580	e-165	
561	e-159	
396	e-109	
382	e-105	
373	e-102	
218	7e-56	
216	2e-55	
209	3e-53	
197	1e-49	
72	7e-12	

Sequences with E-value better than threshold

Sequences producing significant alignments:

Score	E	(bits) Value
33	6.6	
32	7.7	

Sequences with E-value worse than threshold

Alignments

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 584 bits (1505), Expect = e-166  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 580 bits (1505), Expect = e-165  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 561 bits (1505), Expect = e-159  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 396 bits (1505), Expect = e-109  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 382 bits (1505), Expect = e-105  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 373 bits (1505), Expect = e-102  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 218 bits (1505), Expect = 7e-56  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 216 bits (1505), Expect = 2e-55  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 209 bits (1505), Expect = 3e-53  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 197 bits (1505), Expect = 1e-49  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Score = 72 bits (1505), Expect = 7e-12  
 Identities = 328/328 (100%), Positives = 328/328 (100%)

Query: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Subject: 1 NC\_023790.5:14556-151206 (13097516) [AAH03486] Similar to p65 protein [Mus musculus]

Figure 28

NCBI Sequence Viewer - Neiscape 6

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http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=protein&list\_uids=18097516&doctype=GenPept

Home Neiscape Search Bookmarks

1: A003486. Similar to p5 protein [Mus musculus]

LOCUS A003486 328 aa Linear ROD 12-JUL-2001

DEFINITION Similar to p5 protein [Mus musculus].

ACCESSION A003486

VERSION A003486.1 01:1307516

FEATURES

PROTEIN

SOURCE

ORGANISM

Strasbourg R.

Strasbourg R.

Submitted (02-FEB-2001) National Institutes of Health, Human Genome Collection (HGC), Cancer Research Center, National Institutes of Health, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2550.

MT-100 Project URL: <http://www.nci.nih.gov>

Contact: NCI help desk

Email: [ncihelp@nci.nih.gov](mailto:ncihelp@nci.nih.gov)

Tissue Procurement: Lohar Hemighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIM)

RNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Contact: BNC-1000

Web site: <http://www.human-genome.org/CDNA/>

Contact: [villalobos@bnc.edu](mailto:villalobos@bnc.edu)

Villalobos, D.R., Luna, R.A., Balgo, S.M., Balgo, S., Lu, X., Garcia, A.M., Holloway, N., Relford, B., Hodgson, A., Bouch, J., Yu, W., Hurry, D.M., Gibbs, R.A.

Clones distribution: VNC clones distribution information can be found through the I.M.A.G.E. Consortium/ASAC at: <http://imga.llnl.gov>

Series: MAX Plate: 5 Row: 1 Column: 10

Method: conceptual translation

Location/Qualifiers

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/db\_xref="Genbank:U00000"

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/clone\_lib="H1 GCMF MamS"

/lab\_host="H1GCMF"

/notes="Vector: pCMV-SportS"

1..328

/db\_xref="Similar to p5 protein"

1..328

/coded\_by="A003486.1:40..1026"

ORIGIN

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61 tpaiaadll rvlapaine elggrfkyka kffqaaalw rmgvgeada eqiqaers

121 claqkllle dgaavprla halpplqqr qeaeahqg pipktdqqr pglvfmura

181 nuaavkqke captrngpk vepalntst tlvqprnk dggypqrqr tlvqprnk

241 tvaupqqr leaqatqr ggaaylls eldtdanaa dggvadd clldkqps

301 tvaavdkqya eldtdanaa dggypqr

//

RefSeq: October 24, 2001.

Figure 29

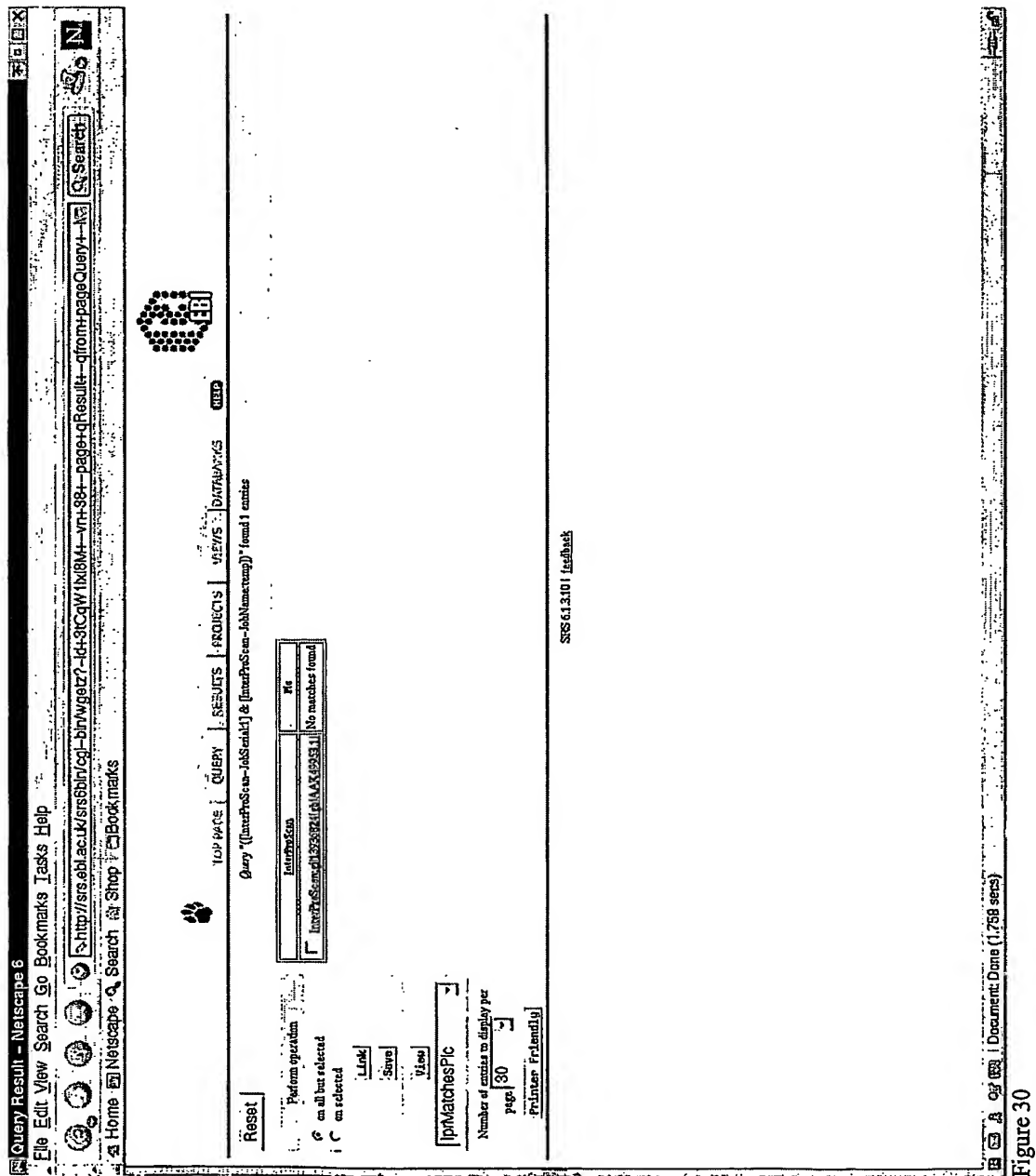
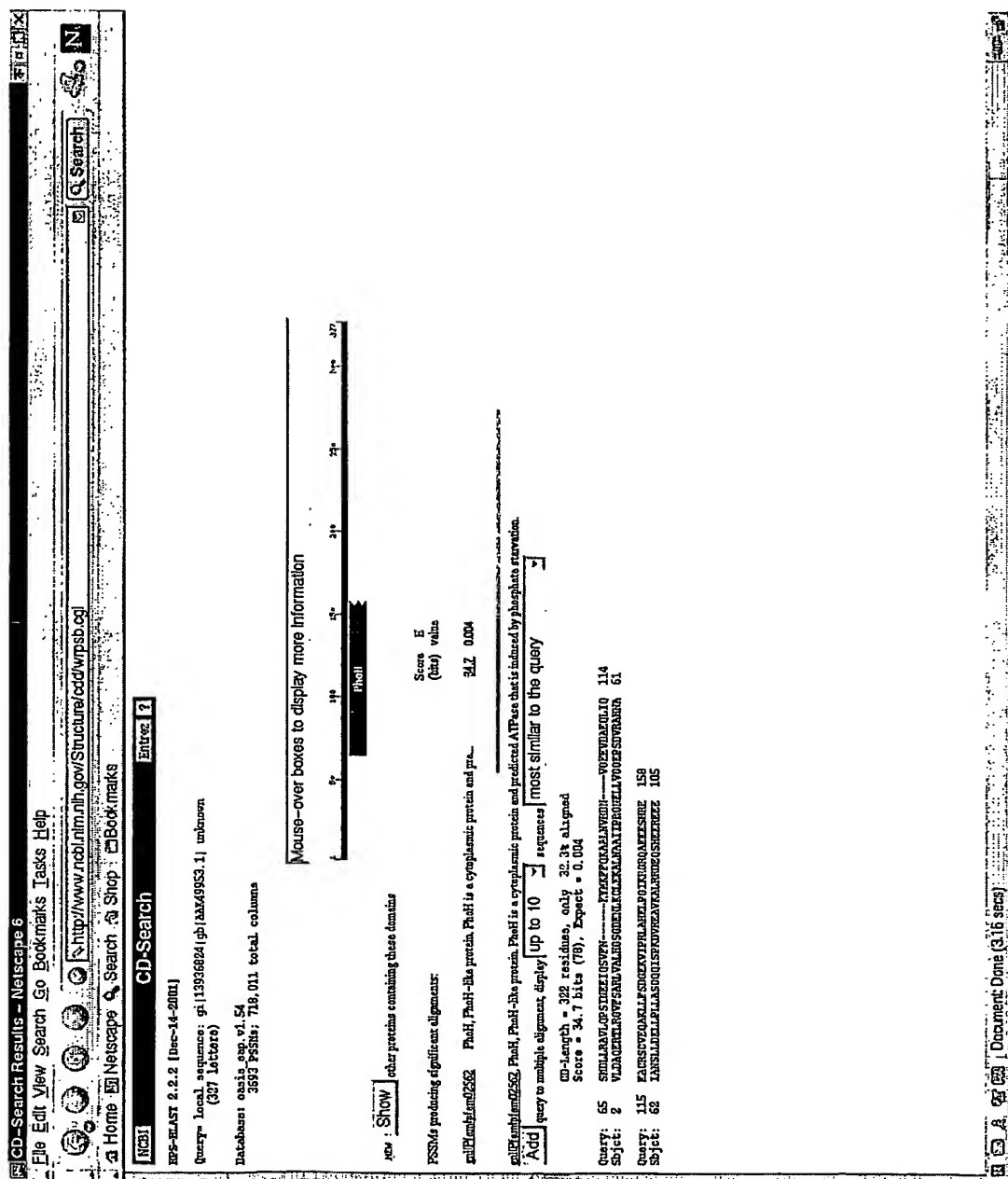
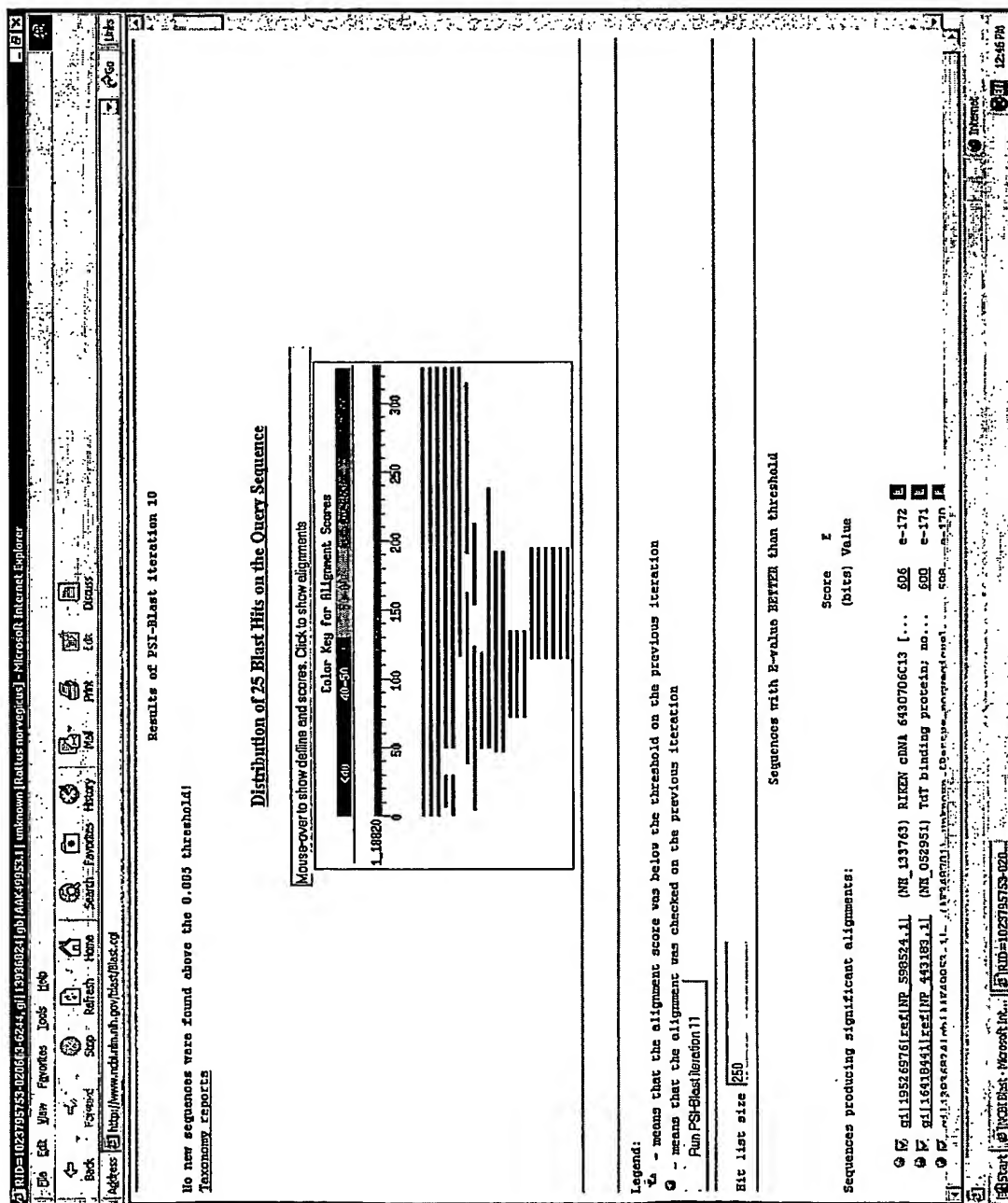
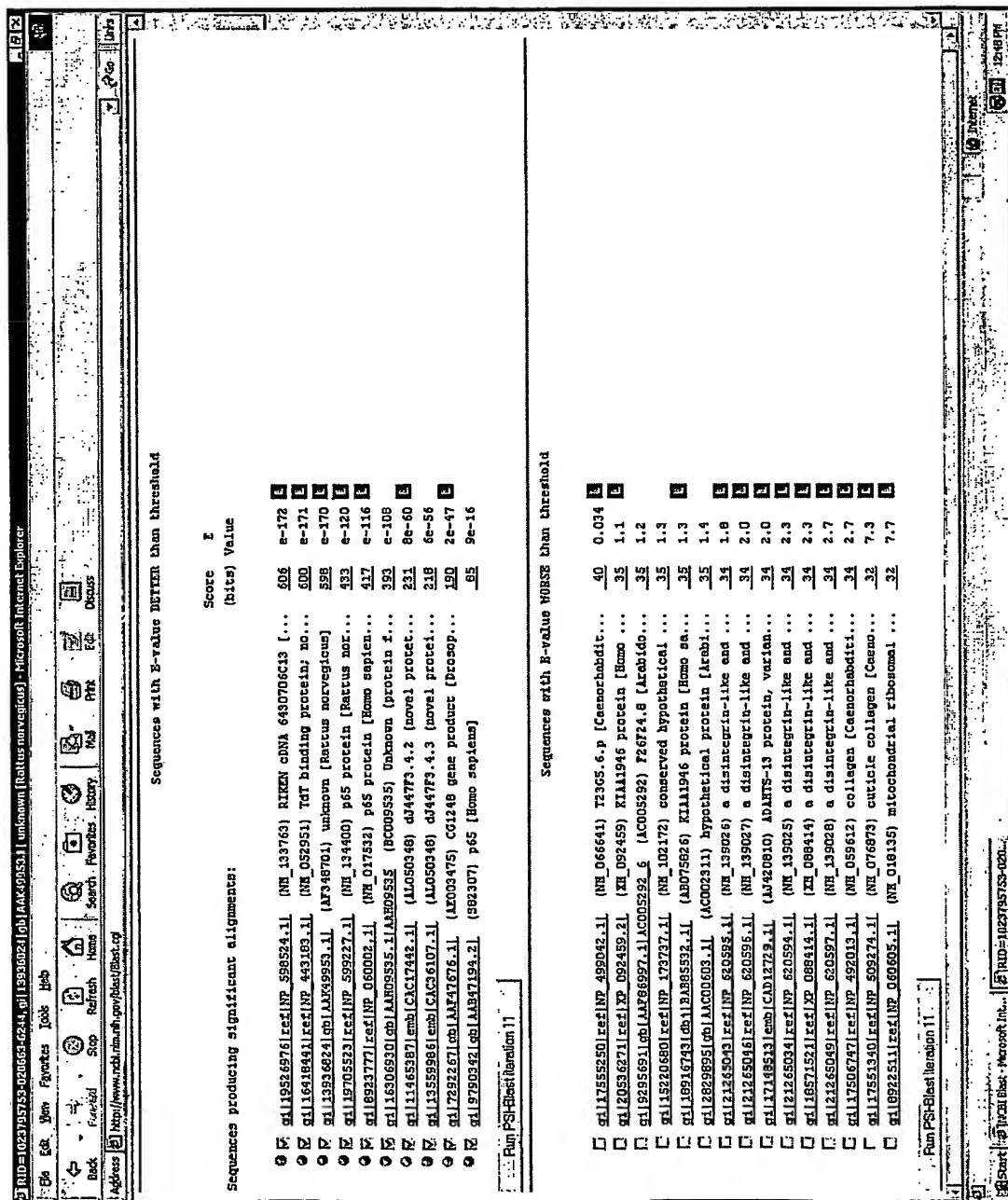


Figure 30



**Figure 31**





[illegible]

### Figure 34

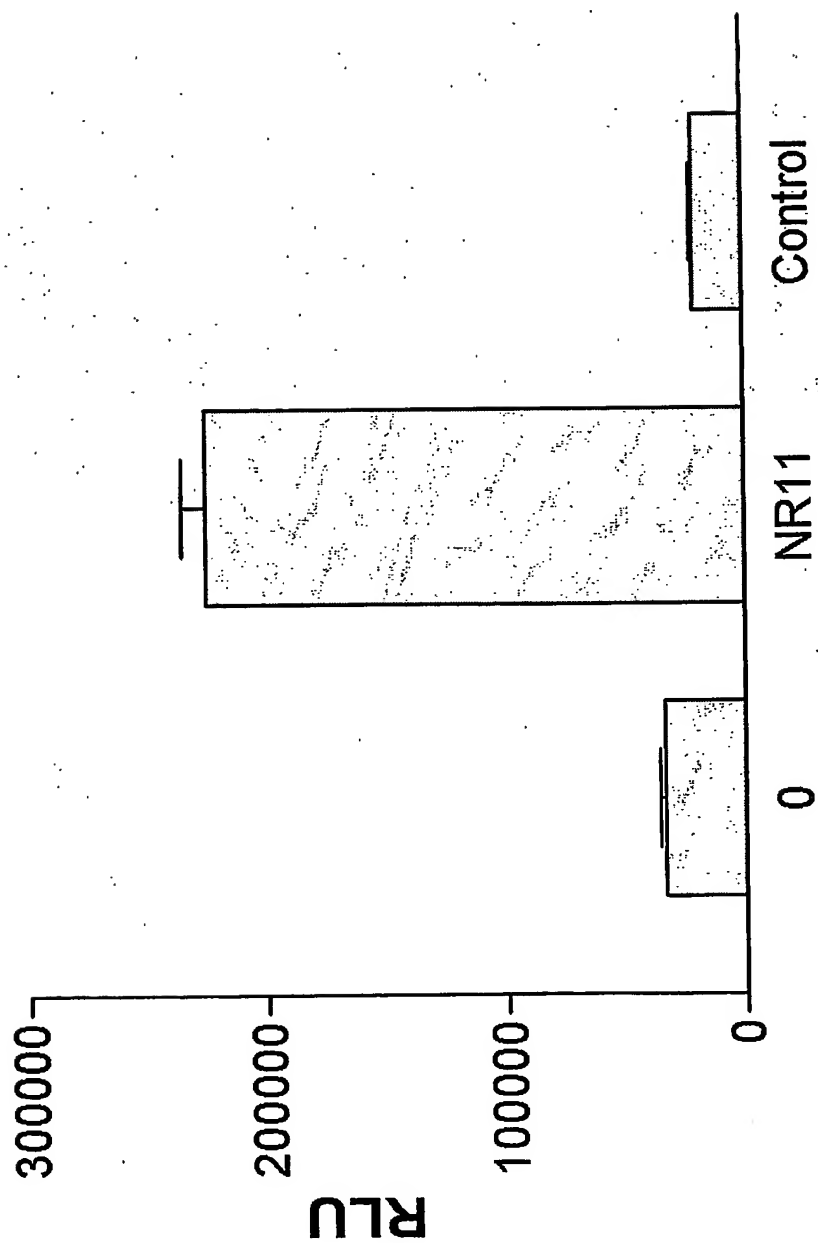


Figure 35

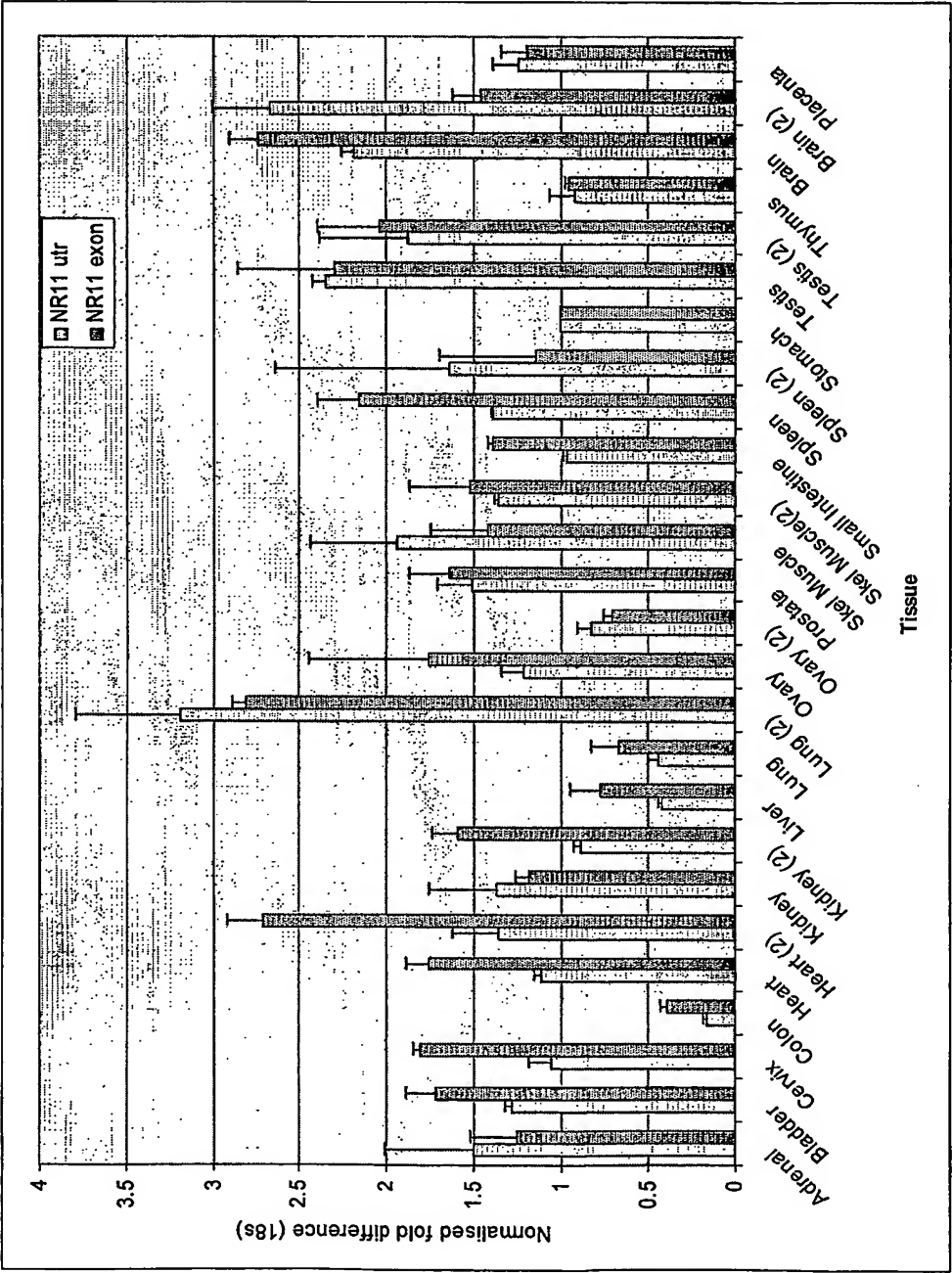


Figure 36

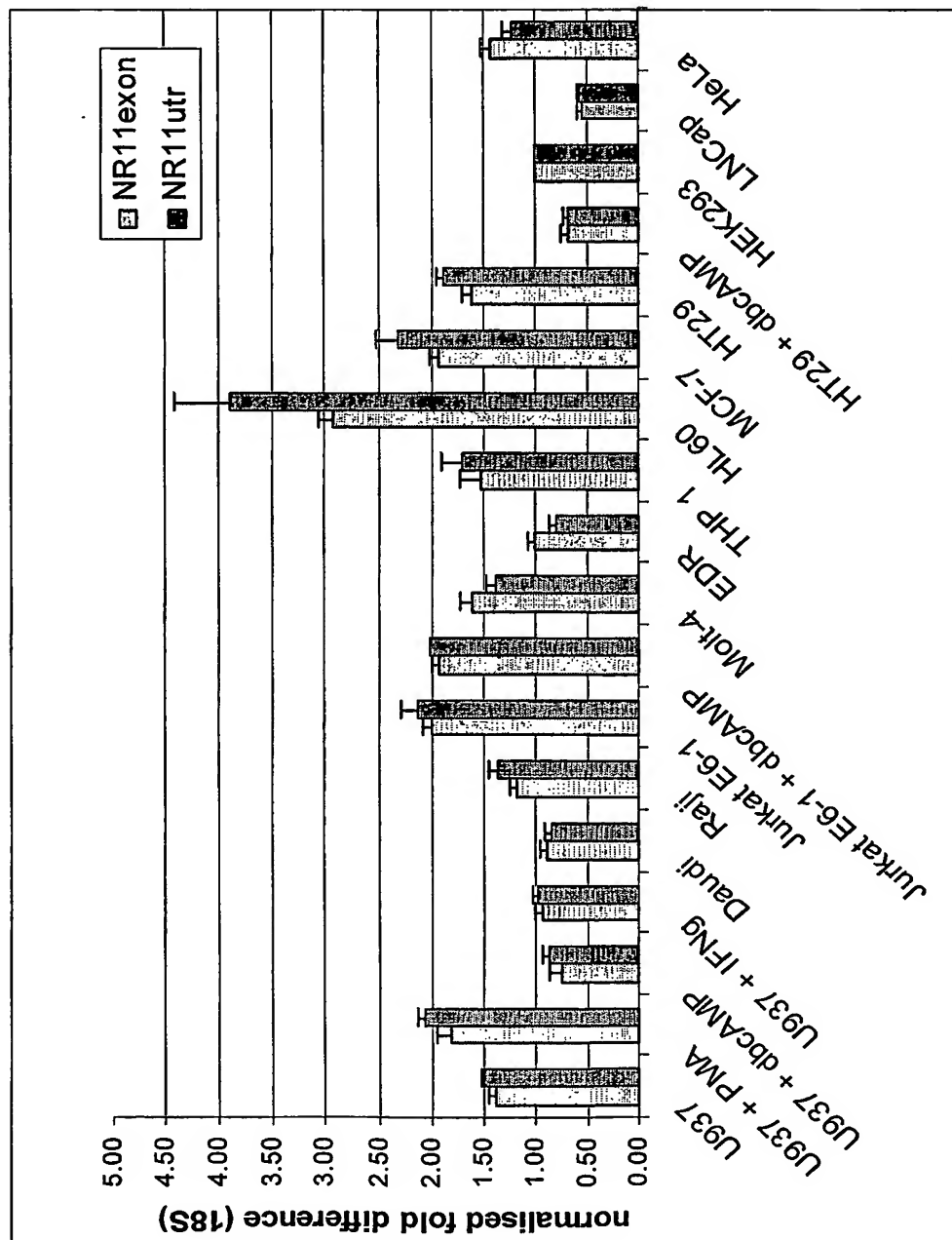


Figure 37

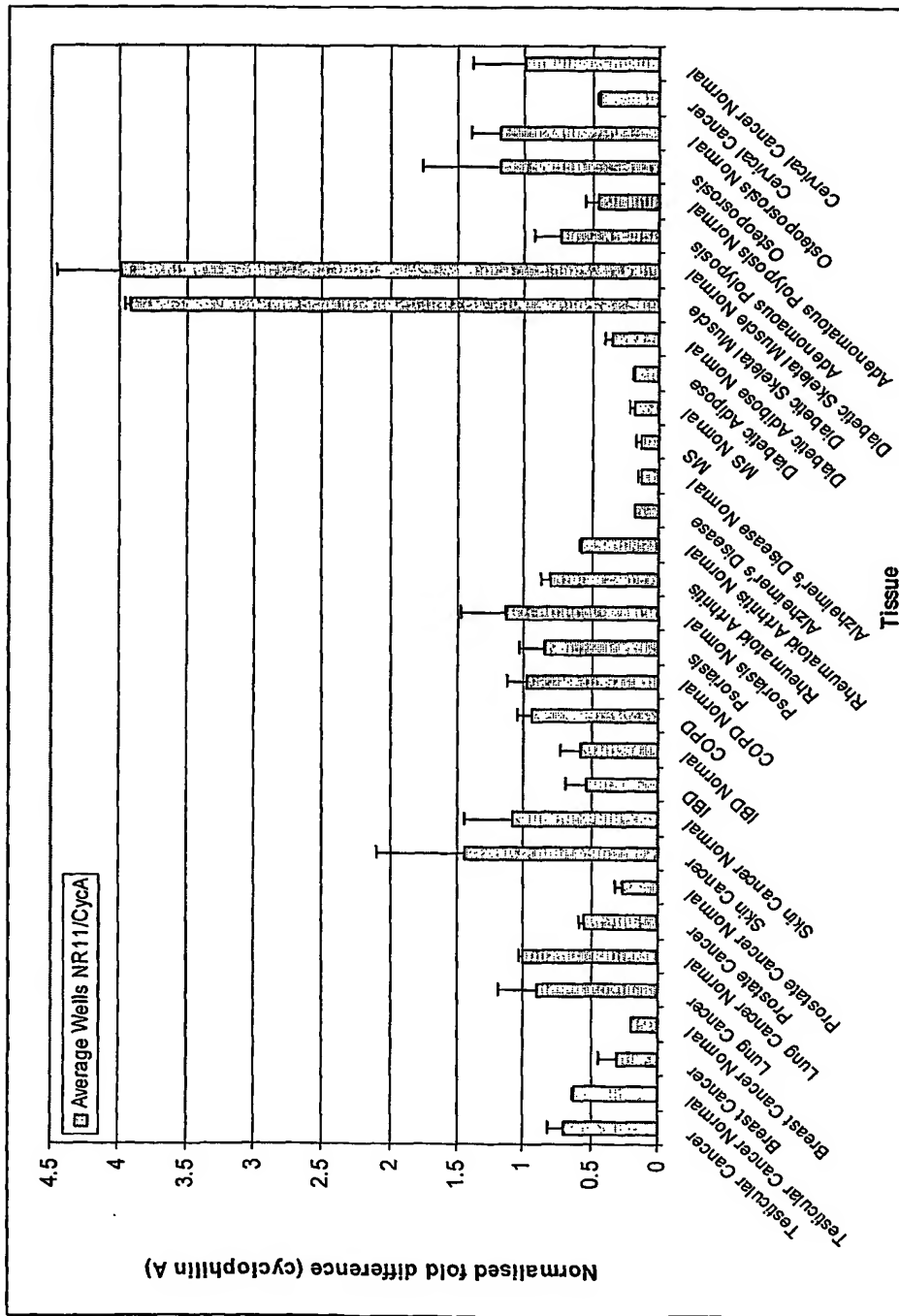


Figure 38

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